

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2003, 02:40:04 : Search time 4460 Seconds  
(without alignments)  
13163.372 Million cell updates/sec

Title: US-09-804-472-1

Perfect score: 3625

Sequence: 1 gaaccagttgtctcagcga.....aaaaaaaaaaaaaaaa 3625

Scoring table: IDENTITY NUC

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estrov:\*  
6: em\_estropl:\*  
7: em\_estro:\*  
8: em\_estro:\*  
9: gb\_estl1:\*  
10: gb\_estl2:\*  
11: gb\_hrc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pin:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	23.9	881	9	AL521597
2	800.6	22.1	865	9	AUI33286
3	798.2	22.0	849	12	BG697014
4	750.4	20.7	1091	14	BM806547
5	747.4	20.6	1154	13	BM542722
6	731.2	20.2	880	9	AI987675

Result	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
1	AL521597	AL521597 LTI_NFL004_NBC2 Homo sapiens CDNA clone CS0DB03YD01 5	AL521597	AL521597.1	GI:12785090	EST.	human.	Human sapiens	Li, W.B., Gruber, C., Jesse, J. and Polyes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	1. .881 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="LTI_NFL004_NBC2" /sex="male" /tissue_type="neuroblastoma cells" /lab_host="DH10B"
2	AL521597	AL521597 LTI_NFL004_NBC2 Homo sapiens CDNA clone CS0DB03YD01 5	AL521597	AL521597.1	GI:12785090	EST.	human.	Human sapiens	Li, W.B., Gruber, C., Jesse, J. and Polyes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	1. .881 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="LTI_NFL004_NBC2" /sex="male" /tissue_type="neuroblastoma cells" /lab_host="DH10B"

# ALIGNMENTS

Result	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
1	AL521597	AL521597 LTI_NFL004_NBC2 Homo sapiens CDNA clone CS0DB03YD01 5	AL521597	AL521597.1	GI:12785090	EST.	human.	Human sapiens	Li, W.B., Gruber, C., Jesse, J. and Polyes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	1. .881 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="LTI_NFL004_NBC2" /sex="male" /tissue_type="neuroblastoma cells" /lab_host="DH10B"
2	AL521597	AL521597 LTI_NFL004_NBC2 Homo sapiens CDNA clone CS0DB03YD01 5	AL521597	AL521597.1	GI:12785090	EST.	human.	Human sapiens	Li, W.B., Gruber, C., Jesse, J. and Polyes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	1. .881 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="LTI_NFL004_NBC2" /sex="male" /tissue_type="neuroblastoma cells" /lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT 271 a 183 c 211 g 215 t 1 others  
ORIGIN

Query Match 23.9%; Score 868; DB 9; Length 881;  
Best Local Similarity 99.7%; Pred. No. 9,1e-97;

Matches 879; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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OY 2074 CCTTAGCTGCTCTGACACAGACAAATATGACATGATATGAAAACATGATTAATG 2133
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Db 1 CCTTAGCTGCTCTGACACAGACAAATATGACATGATATGAAAACATGATTAATG 60

OY 2134 AACACGCTACAAATGATTTCTGTCATTAATGCAAAAAGATTCAGATTAAGGGAT 2193
    |||||||
Db 61 AACACGCTACAAATGATTTCTGTCATTAATGCAAAAAGATTCAGATTAAGGGAT 120

OY 2194 TTGGCTCAGAGAGACCTGCAATTCGCAATGAGAAGTCCAGAAAAAACAGAGGTA 2253
    |||||||
Db 121 TTGGCTCAGAGAGACCTGCAATTCGCAATGAGAAGTCCAGAAAAAACAGAGGTA 180

OY 2254 TCGTTGGCAGTTCGGGTGTTTGGACACGACACCCCTCTCTCCAGCAGAAATC 2313
    |||||||
Db 181 TCGTTGGCAGTTCGGGTGTTTGGACACGACACCCCTCTCTCCAGCAGAAATC 240

OY 2314 CTCGGCATTGAAGCTTGAAGCATTCCTGACATGAGCCCTTTACAGTGCAGACCA 2373
    |||||||
Db 241 CTCGGCATTGAAGCTTGAAGCATTCCTGACATGAGCCCTTTACAGTGCAGACCA 300

OY 2374 CCCCATTGAGATTTGGTGATTTTCCGAAGCTGGGAGCTGAGCAGTCCCTGTAA 2433
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Db 301 CCCCATTGAGATTTGGTGATTTTCCGAAGCTGGGAGCTGAGCAGTCCCTGTAA 360

OY 2434 CTCGCAATGGGCGCTCTGGCATTTATACAAAAAGATTCCTCGGCATTTGGGCC 2493
    |||||||
Db 361 CTCGCAATGGGCGCTCTGGCATTTATACAAAAAGATTCCTCGGCATTTGGGCC 420

OY 2494 AGACGGCAACCAAGACCCGCTTCAATATGTTCAACTGAATCTCAGATGAGAG 2553
    |||||||
Db 421 AGACGGCAACCAAGACCCGCTTCAATATGTTCAACTGAATCTCAGATGAGAG 480

OY 2554 AGAAGAAACGAAAGAGATTTATTTGTTGATAGCAAACTTTTAACTGAGGAGT 2613
    |||||||
Db 481 AGAAGAAACGAAAGAGATTTATTTGTTGATAGCAAACTTTTAACTGAGGAGT 540

OY 2614 CATCTACTTTTTCCTCCCTTACAAAAAGAAATTAATAAAGCCGGGTTTTTG 2673
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Db 541 CATCTAC-TTTTTCCTCCCTTACAAAAAGAAATTAATAAAGCCGGGTTTTTG 599

OY 2674 CAACATGTTTCAAAATATGCTGGTGAATGAGAGATTGTTGGGAGGAAAGAGA 2733
    |||||||
Db 600 CAACATGTTTCAAAATATGCTGGTGAATGAGAGATTGTTGGGAGGAAAGAGA 659

OY 2734 GAGAGAAAGAGAGATGAGATTTTCCCGTCTAACAGAAAGAGGATCAACTCTTATG 2793
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Db 660 GAGAGAAAGAGAGATGAGATTTTCCCGTCTAACAGAAAGAGGATCAACTCTTATG 719

OY 2794 TTTCGCACTGATCATTCAGCTGAGATGCTGATGATGAGAGGCTTGGGCTCAACA 2853
    |||||||
Db 720 TTTCGCACTGATCATTCAGCTGAGATGCTGATGATGAGAGGCTTGGGCTCAACA 779

OY 2854 GAGATGACAGAGAGTCTGAGACACTGGCCTTGTCTCAACATTCGAAAGACATTT 2913
    |||||||
Db 780 GAGATGACAGAGAGTCTGAGACACTGGCCTTGTCTCAACATTCGAAAGACATTT 839

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OY 2914 ATCAGTCCCTATTTCTAGAGGATTAATGATTAATGACCAT 2955  
|||||  
Db 840 ATCAGTCCCTATTTCTAGAGGATTAATGATTAATGACCAT 881

## RESULT 2

AU133286

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: [genomics@hri.co.jp](mailto:genomics@hri.co.jp)

HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix

Research Institute; cDNA library construction; Department of

Virology; Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

Location/Qualifiers

1. 865

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="NT2RP4001717"

/clone\_id="NT2RP4"

/cell\_type="teratocarcinoma"

/cell\_line="NT2"

/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor

cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT 197 a 173 c 212 g 279 t 4 others

ORIGIN

Query Match 22.1%; Score 800.6; DB 9; Length 865;

Best Local Similarity 98.0%; Pred. No. 1,4e-88;

Matches 850; Conservative 0; Mismatches 13; Indels 4; Gaps 4;

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OY 1121 TTTATGAGATCATTTTGTGCTTATGAGGATTTGTTGAGGTCATCAATCC 1180
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Db 1 TTTATGAGATCATTTTGTGCTTATGAGGATTTGTTGAGGTCATCAATCC 60

OY 1181 ATTTGTAACAGCCGCTGCTCTTTTATGAGATCATCAACATGATCACTTTT 1240
    |||||||
Db 61 ATTTGTAACAGCCGCTGCTCTTTTATGAGATCATCAACATGATCACTTTT 120

OY 1241 TGAAGTGTTCCTTTTATTTCTTAAGGGATATTGGAGGCTTTGGGAGCCTTTTCAT 1300
    |||||||
Db 121 TGAAGTGTTCCTTTTATTTCTTAAGGGATATTGGAGGCTTTGGGAGCCTTTTCAT 180

OY 1301 TAGGGCAAAATTTCCCTGCTGCTGTCGACGCAAGTCCACGAAATTTGGAAATGCCGT 1360
    |||||||
Db 181 TAGGGCAAAATTTCCCTGCTGCTGTCGACGCAAGTCCACGAAATTTGGAAATGCCGT 240

OY 1361 TCTGAGAGTCAATTAATTTGTCGAGCATTACTGCTGTATAGCCTTCCCTAATCCATAC 1420
    |||||||
Db 241 TCTGAGAGTCAATTAATTTGTCGAGCATTACTGCTGTATAGCCTTCCCTAATCCATAC 300

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QY	1945	CGTTGGCAGGGAAGGCAATTATTAAGACACACATCCGATTAATGGAATACCCCTTTCTGG	200
Db	2	CGTTGGCAGGGAAGGCAATTATTAAGACACACATCCGATTAATGGAATACCCCTTTCTGG	61
QY	2005	ATGCAAAAGAAGAAATTCATCTCATATCCACCCTGGCTGCTGCTATGAGACCTCGAAGA	206
Db	62	ATGCAAAAGAAGAAATTCATCTCATATCCACCCTGGCTGCTGCTATGAGACCTCGAAGA	121
QY	2065	ATGATCTCTCCCTTAGCTGCTCCTACACAGACAAATATGACAGTGGATGATATGAAGAA	212
Db	122	ATGATCTCTCCCTTAGCTGCTCCTACACAGACAAATATGACAGTGGATGATATGAAGAA	181
QY	2125	TGATTAATGAACACAGCTACAAATGGAATTTCTGTCAATATGTCAAAAGAAATTCAGAG	218
Db	182	TGATTAATGAACACAGCTACAAATGGAATTTCTGTCAATATGTCAAAAGAAATTCAGAG	241
QY	2185	TAGTGGAGATTTGCCCTCAGAGAGACCTGACAAATTCGAATAGAAAGTGCAGAGAAAA	224
Db	242	TAGTGGAGATTTGCCCTCAGAGAGACCTGACAAATTCGAATAGAAAGTGCAGAGAAAA	301
QY	2245	AAGAAGATTCGTTGGAGAGTTCGGGTGTGTTTGCACAGACACCCCATCTCTTCAG	230
Db	302	AAGAAGATTCGTTGGAGAGTTCGGGTGTGTTTGCACAGACACCCCATCTCTTCAG	361
QY	2305	CAGAAAGTCTCGGCCATTGGAAGCTTCGAAGCATTCGTACATGAGCCCTTTTACAGTA	236
Db	362	CAGAAAGTCTCGGCCATTGGAAGCTTCGAAGCATTCGTACATGAGCCCTTTTACAGTA	421
QY	2365	CAGACCCACACCCCAATGAGAGATGTGTGATATTTTCCGAAAGCTGGAGCTGAGGCACT	242
Db	422	CAGACCCACACCCCAATGAGAGATGTGTGATATTTTCCGAAAGCTGGAGCTGAGGCACT	481
QY	2425	GCCTTGTAACCTCAATGAGGCGCCTCTTGGCATTTATACAAAAGAAAGATATCCGCGC	248
Db	482	GCCTTGTAACCTCAATGAGGCGCCTCTTGGCATTTATACAAAAGAAAGATATCCGCGC	541
QY	2485	ATATGGCCACGAGCGCAACCAAGACCCGCTTCATATAATGTTCAACTGAATCTCACAGA	254
Db	542	ATATGGCCACGAGCGCAACCAAGACCCGCTTCATATAATGTTCAACTGAATCTCACAGA	601
QY	2545	TGAGAGAGAGAAAGAAACGGAAGAGAAGTTATTTGTTGAATAGCACACATCTTTAAAC	260
Db	602	TGAGAGAGAGAAAGAAACGGAAGAGAAGTTATTTGTTGAATAGCACACATCTTTAAAC	661
QY	2605	TGAGAGAGATATCTACTTTTCTTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	266
Db	662	TGAGAGAGATATCTACTTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	721
QY	2664	C-GGGTTTTGCAACATG- -TTTGCAAATATATGCTGTGGAATGAGAGAGTGTGTTGG	2720
Db	722	CGGGTTTTTGCACATGAGTTTGCACAAATATATGCTGTGGAATGAGAGAGTGTGTTGG	781
QY	2721	GAGGGAAG- - - - -AGAGAGAGAGAAAGAGAGTGTGTTTCCGCTCTACACAGAAAGA	2775
Db	782	GAGGGAAGAGAGAAACAAAGACACAGCGGCTGACGTTATTTTCCCGCTTACAGGAAACA	841
QY	2776	GCGATAT- -AACTCCTATATGTTTGCACACTGGA- -TGCATTCAGCTGAGAGATGCTCT	2828
Db	842	GCGATATCTACTCTATCGTCTTGCACTGAGCTGACTTACGCGCTGAGAGATGCTCT	896

REFERENCE	SEQUENCE	FEATURES
1 (bases 1 to 880)	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
1	Marra,M., Hillier,L., Kucoba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuck,R., Riller,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.	
JOURNAL	The Mashu-NCI Mouse EST Project 1999	
COMMENT	Unpublished (1999) Contact: Marra M/Mashu-NCI Mouse EST Project 1999 Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNLN : contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1003862 Seq primer: custom primer used High quality sequence stop: 509.	
FEATURES	Location/Qualifiers	
source	1..880	
	/organism="Mus musculus"	
	/strain="C57BL"	
	/db_xref="taxon:10090"	
	/clone="IMAGE:2182194"	
	/clone_lib="Sugano mouse kidney mk1a"	
	/sex="female"	
	/dev_stage="adult"	
	/lab_host="DH10B"	
	/note="Organ: kidney; Vector: pME18S-FL3; Site:1: DraIII (CACTGTGTG); Site:2: DraIII (CACCAATGTC); 1st strand cDNA was primed with an oligo(dT) primer	
	[ATGCGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor (TTGTGGCCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCAATGTC). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTTCGCTCTAAACACTGGC and 3' end primer CGACCTCGACCTGACACA."	
BASE COUNT	237 a 214 c 181 g 247 t 1 others	
ORIGIN		
Query Match	20.2%; Score 731.2; DB 9; Length 880;	
Best Local Similarity	90.3%; Pred. No. 3.7e-80;	
Matches 792; Conservative	0; Mismatches 84; Indels 1; Gaps 1.	
QY	1756 AGTGTGTGAGGTGGGGGCTGATTTTCATTACAC--TGCGCTTATGCCATGGTGGTCT 1814	
DB	880 AGTGTGTAAAGTGGGGGCTGACCTCACACCTCCAGGGGCTTATGCCCATGTGGGGGCT 821	
QY	1815 GCTGCATGCTTAGTGGTGTGTGCACAAGATGACTGTCTCCCTGGTGGTTATGTTTTGAG 1874	
DB	820 GCTGCGTCTTAGATAGTGTGTGCACAAGATGACTGTCTCTGCTGGTTATGTTTTGCA 761	
OY	1875 CTTACTGGAGGCTTGAGATATATTTGTCCCTTATAGCTGCAGTCATGACCAAGTAATGG 1934	
DB	760 CTTACTGGAGGCTTGAGATATATTTGTCTCTTATAGCTGCAGTAATGACCAAGTAATGG 701	

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OY 1935 GTTGAGATGCTTTGGCAGGGAAGCATTTATGAAACACATCCGATTAAATGATAC 1994
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 700 GTTGATGATGCTTTGGTGGTGAAGGATTTATGAAACACATCCGATTAAATGATAC 641
OY 1995 CTTTCTTGATGCAAAAGAAATTCATCATACCCCTGGTGGTGGATATGAGA 2054
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Db 640 CTTTCTTGATGCAAAAGAAATTCATCATACCCCTGGTGGTGGATATGAGA 581
OY 2055 CTTGAGAGATGCTTTGCTCCCTTGTCTGCTGACAGAGCAATATGACAGTGGATGAT 2114
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 580 CTTGAGAGATGCTTTGCTCCCTTGTCTGCTGACAGAGCAATATGACAGTGGATGAC 521
OY 2115 ATAGAAATCATGATTAAATGAAACAGCTACATGATTTCTGTCATATGTCAGAAAGAA 2174
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 520 ATAGAAATCATGATTAAATGAAACAGCTACATGATTTCTGTCATATGTCAGAAAGAA 461
OY 2175 TCTCAGAGATTTAGTGGATTTGCCCTCAGAGAGACCTGACATATGAAATGAAAGTGGC 2234
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 460 TCTCAGAGATTTAGTGGATTTGCCCTCAGAGAGACCTGACATATGAAATGAAAGTGGC 401
OY 2235 AGGAAAAACAGAGAGGATTCGTTGGCAGTTCTGGGTTGTCACAGACACACCCCA 2294
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 400 AGGAAAAACAGAGAGGATTTGTTGGCAGTTCTGGGTTGTCACAGACATCTCCA 341
OY 2295 TCTCTTCAGCAGAGAAAGTCTCGGCAATTTGAAGCATTTCTTACATGAGCCCT 2354
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 340 TCTCTTCAGCAGAGAAAGTCTCGGCAATTTGAAGCATTTCTTACATGAGCCCT 281
OY 2355 TTACAGTACAGACACACCCCAATGAGATTTGTGTGATATTTCCGAAAGCTGGGA 2414
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 280 TTACAGTACAGACACACCCCAATGAGATTTGTGTGATATTTCCGAAAGCTGGGT 221
OY 2415 CTGAGGAGATGCTTTGTAATCTCAATATGAGGCTCTTGGCATTTATGAAAGAAAGAT 2474
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Db 220 CTGAGGAGATGCTTTGTAATCTCAATATGAGGCTCTTGGCATTTATGAAAGAAAGAT 161
OY 2475 ATCTCTCGCATATGATGCCCAAGAGGCAACCAAGACCCCTTCAATATATGTTCACTGA 2534
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Db 160 ATCTCTCGCATATGATGCCCAAGAGGCAACCAAGACCCCTTCAATATATGTTCACTGA 101
OY 2535 ATCTCAGATGAGAGAGAGAGAAAGCAAGAGGAAATTTATTTGTTAAATAGCAAA 2594
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 GTCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 41
OY 2595 CTCTTTACCTGAGGAGGATCATCTACTTTTCTTCT 2631
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Db 40 TCTCTTAATCTGGGAGCTGGCCACTTTTCTCTCT 4

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RESULT 7
AUI19689 830 bp mRNA linear EST 01-AUG-2002
LOCUS AUI19689 HEMBA1 Homo sapiens cDNA clone HEMBA1006412 5', mRNA
DEFINITION
sequence.
ACCESSION AUI19689
VERSION AUI19689.1 GI:10934924
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
  1 (bases 1 to 830)
  Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
  Yamamoto,J., Makamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
  Iwagaki,T.
  HRI human cDNA project
  Unpublished (2000)
  Contact: Takao Iwagaki
  Genomics Laboratory
  Helix Research Institute
  1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
  Tel: 81-438-52-3975
  Fax: 81-438-52-3986

```

Email: [genomics@hri.co.jp](mailto:genomics@hri.co.jp)  
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix  
 Research Institute; cDNA library construction; Department of  
 Virology, Institute of Medical Science, University of Tokyo, and  
 Helix Research Institute.

#### FEATURES

source  
 1. 830  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="HEMBA1006412"  
 /clone\_1lb="HEMBA1"  
 /tissue\_type="whole embryo, mainly head"  
 /dev\_stage="embryo, 10 weeks"  
 /note="vector: pME18SFL3"  
 BASE COUNT 226 a 158 c 189 g 254 t 3 others  
 ORIGIN

Query Match 19.2%; Score 697.6; DB 9; Length 830;  
 Best Local Similarity 98.1%; Pred. No. 4.6e-76;  
 Matches 706; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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OY 418 CAGCATGGAAATGACAAAGTTTATGATGCTGCTGACAGATGGCTACTATACAC 477
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Db 1 CAGCATGGAAATGACAAAGTTTATGATGCTGCTGACAGATGGCTACTATACAC 60
OY 478 TAACAGATTTGGCATTCAGGGGCACTGGCCGATTAAATAGACATTTGCTGATGATGA 537
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TAACAGATTTGGCATTCAGGGGCACTGGCCGATTAAATAGACATTTGCTGATGATGA 120
OY 538 CTGACCTTAAGAGAGGCAATTTGCCCTTAGTGTGCTGTACCAACAGCAAGTGTCTT 597
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Db 121 CTGACCTTAAGAGAGGCAATTTGCCCTTAGTGTGCTGTACCAACAGCAAGTGTCTT 180
OY 598 GGGGATCTAATGAACACACATTTGAAGAGAGGATTAATGTCACAGTGGAAAAATGGG 657
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GGGGATCTAATGAACACACATTTGAAGAGAGGATTAATGTCACAGTGGAAAAATGGG 240
OY 658 CAGAAATTAATCATAGTCAAGCAGAGAGGCTGCTGTTCTTAATCATGACATATATGT 717
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Db 241 CAGAAATTAATCATAGTCAAGCAGAGAGGCTGCTGTTCTTAATCATGACATATATGT 300
OY 718 ACATCTTCTGGGCTTGATGTTTGGCTTCTTGACATTTCCCTGTAAGCTATTTGCTC 777
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 ACATCTTCTGGGCTTGATGTTTGGCTTCTTGACATTTCCCTGTAAGCTATTTGCTC 360
OY 778 CATATGCTGTGGCTGCGAATTCAGAGATTAACATATTTAAGGAGTCAATCATCA 837
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Db 361 CATATGCTGTGGCTGCGAATTCAGAGATTAACATATTTAAGGAGTCAATCATCA 420
OY 838 GAGGTACTTGGGAAATGAGCTTTAATGATTAACCATCATATGATGCTGCTGCTG 897
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 GAGGTACTTGGGAAATGAGCTTTAATGATTAACCATCATATGATGCTGCTGCTG 480
OY 898 CATCAGCTTGTAGTTAGAGAAAGAGTCCCTGTAATGTTGCTGCTGCTGCGGAA 957
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Db 481 CATCAGCTTGTAGTTAGAGAAAGAGTCCCTGTAATGTTGCTGCTGCTGCGGAA 540
OY 958 ATATCTTCTGCTACCTGTTCCAAAGATATAGCAACAAAGCAAGCTAAAGAGAGTGC 1017
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 ATATCTTCTGCTACCTGTTCCAAAGATATAGCAACAAAGCAAGCTAAAGAGAGTGC 600
OY 1018 TATCAGCTGCTCAGCTGCAAGGGGTTTCTGATCTTTGGTGCACCAATTTGAGAGATTG 1077
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 TATCAGCTGCTCAGCTGCAAGGGGTTTCTGATCTTTGGTGCACCAATTTGAGAGATTG 660
OY 1078 TTTTATGCTGGAAGAGTTAGCTATTTATTTCTCTCAAACTTTATGAGATCATTTT 1137
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 661 TTTTATGCTGGAAGAGTTAGCTATTTATTTCTCTCAAACTTTATGAGATCATTTT 720

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RESULT 8
AM009467/c 740 bp mRNA linear EST 08-MAR-2000
LOCUS AM009467

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Query Match 18.2%; Score 660.6; DB 9; Length 735;  
 Best Local Similarity 95.8%; Pred. No. 1.6e-71;  
 Matches 704; Conservative 0; Mismatches 26; Indels 5; Gaps 3;

QY 1247 GTTTCCTTTATTTCTTCTAGGGTATTTGAGGGCTTTGGGAGCCCTTTTTCATTAAGGCG 1306  
 1 GTTTCCTTTATTTCTTCTAGGGTATTTGAGGGCTTTGGGAGCCCTTTTTCATTAAGGCG 60

QY 1307 AAATATGCGGTGTGTGTCAGCAGTCCAGCAAAATTTGGAAGTATCCCGTTCGGA 1366  
 61 AAATATGCGGTGTGTGTCAGCAGTCCAGCAAAATTTGGAAGTATCCCGTTCGGA 120

QY 1367 AGTCATTATTTCTTCTAGCAGCATTACTGTGTGATAGCCCTTCCATTCATCAGTAGGCT 1426  
 121 AGTCATTATTTCTTCTAGCAGCATTACTGTGTGATAGCCCTTCCATTCATCAGTAGGCT 180

QY 1427 AAACACAGTGAAGTATCAAAAGAGCTTTTACAGACTGTGTCCCTCGAATCCCTCTTC 1486  
 181 AAACACAGTGAAGTATCAAAAGAGCTTTTACAGACTGTGTCCCTCGAATCCCTCTTC 240

QY 1487 TCTTTGACTACAGAAATGATGAAATGCCAATAATTTGATGATGATGATGATGATGATG 1546  
 241 TCTTTGACTACAGAAATGATGAAATGCCAATAATTTGATGATGATGATGATGATGATG 300

QY 1547 TCCAGCAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1606  
 301 TCCAGCAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360

QY 1607 AATCATATGACAGTATTTACATTTTGGCATCAAGTTCATCAGGCTTTGATCCAGCAG 1666  
 361 AATCATATGACAGTATTTACATTTTGGCATCAAGTTCATCAGGCTTTGATCCAGCAG 420

QY 1667 CATGGCATTGAGCAGATGCGAGAGAGATGCGGGATGCGGGAGCAGCTTGCTTA 1726  
 421 CATGGCATTGAGCAGATGCGAGAGAGATGCGGGATGCGGGAGCAGCTTGCTTA 480

QY 1727 CTATACACAGCAGTGTATCTTTAAGAGTGTGTGAGTGTGCGGGCTGATTCATTTAC 1786  
 481 CTATACACAGCAGTGTATCTTTAAGAGTGTGTGAGTGTGCGGGCTGATTCATTTAC 540

QY 1787 ACCGCGCTTTATGCCATGTTGGTGTGCTGCTGATGCTTACAGTGTGCTG-TCACAAGATGA 1845  
 541 ACCGCGCTTTATGCCATGTTGGTGTGCTGCTGATGCTTACAGTGTGCTG-TCACAAGATGA 600

QY 1846 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1904  
 601 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

QY 1905 CTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1961  
 661 CTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720

QY 1962 ATTTATGAGAGACAC 1976  
 721 ATTTATGAGAGACAC 735

RESULT 10  
 BO960629 891 bp mRNA linear EST 21-AUG-2002  
 LOCUS BO960629  
 DEFINITION AECN00UR\_8932469 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:6468812  
 5', mRNA sequence.  
 ACCESSION BO960629  
 VERSION BO960629.1 GI:22376107  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 891)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999).  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabsp@email.nih.gov  
 Tissue Procurement: The Cepko Laboratory  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 plate: LHAM3996 row: 0 column: 21  
 high quality sequence stop: 671.  
 Location/Qualifiers  
 1. 891  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6468812"  
 /clone\_id="NIH\_MGC\_94"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="organ: eye; Vector: pCMV-SPORT6; Site:1: NotI;  
 Site:2: SalI; Cloned unidirectionally; oligo-dt primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

BASE COUNT 278 a 183 c 209 g 218 t 3 others

ORIGIN

Query Match 18.2%; Score 660.6; DB 14; Length 891;  
 Best Local Similarity 85.8%; Pred. No. 1.4e-71;  
 Matches 757; Conservative 0; Mismatches 117; Indels 8; Gaps 2;

QY 1920 ATGACCAAGTAATGGTGTGAGATGCTTTGGAGGAGGAGCATTATTAAGCACACATC 1979  
 2 ATGACCAAGTAATGGTGTGAGATGCTTTGGAGGAGGAGCATTATTAAGCACACATC 61

QY 1980 CGATTAAATGGATACCTTTCTTGATGCAAGAGAGATTTACTATCAACCTGGCT 2039  
 62 CGATTAAATGGATACCTTTCTTGATGCAAGAGATTTACTATCAACCTGGCT 121

QY 2040 GCTGACCTTATGACAGCTCGAAGAGATGATGATGATGATGATGATGATGATGATGATG 2099  
 122 GCTGATGTTATGACAGCTCGAAGAGATGATGATGATGATGATGATGATGATGATGATG 181

QY 2100 ATGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2159  
 182 ATGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 241

QY 2160 ATATATGCAAAAGATCTCAGAGATTTAGTGGATTTGCTCCAGAGAGACCTCAAT 2219  
 242 ATATATGCAAAAGATCTCAGAGATTTAGTGGATTTGCTCCAGAGAGACCTCAAT 301

QY 2220 GCAATGAGAAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2279  
 302 GCAATGAGAAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 361

QY 2280 GCACAGCAGACCCCATCTCTTCCAGAGAGAAAGCTGCGGCTTGAAGCTTGAAGAT 2339  
 362 GCACAGCAGTACCTCTCTTCCAGAGAGAAAGCTGCGGCTTGAAGCTTGAAGAT 421

QY 2340 CTGACATGAGCCCTTTTACAGTACAGACACACACCCCAATGAGATTTGGATAT 2399  
 422 CTGACATGAGCCCTTTTACAGTACAGACACACCCCAATGAGATTTGGATAT 481

QY 2400 TTCCGAAAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2459  
 482 TTCCGAAAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 541

QY 2460 ATACCAAAAAAGATATCTCCGATATGAGCCAGAGGAGGAGGAGGAGGAGGAGGAGG 2519  
 542 ATACCAAAAAAGATATCTCCGATATGAGCCAGAGGAGGAGGAGGAGGAGGAGGAGG 601

QY 2520 ATATATGTTCAAGTATCTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 2579



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Db 602 AATATGTTCAACTGAGTCCTGTAGATGAGACAGAGAGACAGAAAGAAAGTTCCGT 661
Oy 2580 TGTGTAATGACCACTCTTTTAACTGAGGAGATCTACTTTTTTTCCTTCCTTACA 2639
Db 662 TGTGTAATGACCACTCTTTTAACTGAGGAGATCTACTTTTTTTCCTTCCTTACA 721
Oy 2640 AAAAAAGAAAGAAATATTAAGACCGGTTTTCACATGTTTTCACAAATATGCTGCT 2699
Db 722 AAAAAAGAAAGAAATATTAAGACCGGTTTTCACATGTTTTCACAAATATGCTGCT 779
Oy 2700 GGAATGAGAGCTTGTGTTGGGAGGAGAAAGAGAGAAAGAAAGATGATTTTCC 2759
Db 780 AGAGCAAGAGGATGTTGTTGGGAGGAGG-----GAGAGAGGAGAAAGATGATTTTCC 833
Oy 2760 CCTTACAGAAAGACGCTATCACTCTCTATTTGTTCTGCAC 2801
Db 834 CTAGCTACCTGGAGCAAGNNAATCATCTCATGTGCTCTGCAC 875

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RESULT 11
AL042683 730 bp mRNA linear EST 29-FEB-2000
LOCUS DKEZp434P0121_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION DKEZp434P0121 5', mRNA sequence.
ACCESSION AL042683
VERSION AL042683.1 GI:5422132
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE 1 (bases 1 to 730)
AUTHORS Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Blum H
MIPS

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AM Kioferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No sl sequence available.
This clone (DKEZp434P0121) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

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FEATURES
source 1..730

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKEZp434P0121"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"

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BASE COUNT 221 a 166 c 164 g 177 t 2 others
ORIGIN
Query Match 18.2% Score 660; DB 9; Length 730;
Best local similarity 98.1%; Pred. No. 1.8e-71;
Matches 679; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

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Oy 2014 AAGATTCATCATACACCCCTGGCTGCTGACGTTATGAGACCTCGAAGATGATCTC 2073
Db 39 AGCGGTCCTCATACACCCCTGGCTGCTGACGTTATGAGACCTCGAAGATGATCTC 98
Oy 2074 CCTTACTCTCTGACACAGGACATATATGACAGTATATAGAAACATGATTATG 2133
Db 99 CCTTACTCTCTGACACAGGACATATATGACAGTATATAGAAACATGATTATG 158

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Oy 2134 AAGACAGCTACATGATGATTTTCTGTCATATGTCACAAAGATCTGAGATTAGTGGAT 2193
Db 159 AAGACAGCTACATGATGATTTTCTGTCATATGTCACAAAGATCTGAGATTAGTGGAT 218
Oy 2194 TTGCCCTCAGAGAGACCTGCAATTTGCAATAGAAAGTCCAGAGAAAGAAAGAGTA 2253
Db 219 TTGCCCTCAGAGAGACCTGCAATTTGCAATAGAAAGTCCAGAGAAAGAAAGAGTA 278
Oy 2254 TCGTTGGCAGTTCTCGGGTGTGTTTGGACAGCAGACCCCATCTCTTCCAGAGAAAGTC 2313
Db 279 TCGTTGGCAGTTCTCGGGTGTGTTTGGACAGCAGACCCCATCTCTTCCAGAGAAAGTC 338
Oy 2314 CTGGCCATTGGAAGCTTCAACATCTTACATGAGCCCTTTTACAGTACAGACACACA 2373
Db 339 CTGGCCATTGGAAGCTTCAACATCTTACATGAGCCCTTTTACAGTACAGACACACA 398
Oy 2374 CCCCAGTGAAGATGTTGTTGATATTTTCCGAAAGCTGAGACTGAGCAGTCCCTGTAA 2433
Db 399 CCCCAGTGAAGATGTTGTTGATATTTTCCGAAAGCTGAGACTGAGCAGTCCCTGTAA 458
Oy 2434 CTCACATGAGGCGCCCTCTTGGCATTATACAAAGATATCTCTCCGCAATATGCGCC 2493
Db 459 CTCACATGAGGCGCCCTCTTGGCATTATACAAAGATATCTCTCCGCAATATGCGCC 518
Oy 2494 AGACGGCAACACAGACCCCGCTTCAATATGTTCACTGATCTCAGATGAGAGAG 2553
Db 519 AGACGGCAACACAGACCCCGCTTCAATATGTTCACTGATCTCAGATGAGAGAG 578
Oy 2554 AGAGAAAGAGAGAGAGAGATTTATTTGTTGAATAGACACACTTTTAACTGAGGAGCT 2613
Db 579 AGAGAAAGAGAGAGAGAGATTTATTTGTTGAATAGACACACTTTTAACTGAGGAGCT 638
Oy 2614 CATCTACTTTTCTCTCTCTCTTACAAAAAGAAAGG---AATATTAAGCGGGGTTT 2670
Db 639 CATCTACTTTTCTCTCTCTCTTACAAAAAGAAAGGAAATATTAAGAAAGCGGGGTTT 698
Oy 2671 TTGCAACATGTTTTCGCAATATGCTGTGTA 2702
Db 699 TTGCAACATGTTTTCGCAATATGCTGTGTA 730

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RESULT 12
AA551133/c 673 bp mRNA linear EST 09-SEP-1997
LOCUS nk75h01.s1 NCI-CGAP Sch1 Homo sapiens cDNA clone IMAGE:1019377 3'
DEFINITION similar to TR:G929680 G929680 CLC4. ; mRNA sequence.
ACCESSION AA551133
VERSION AA551133.1 GI:2321385
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 673)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc., David B. Kitzman,
Ph.D.

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cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 1026 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 401.

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QY 3310 GCGAAGCAAAATCTCTCATTTGTGCGCTGCTCAAAAACCAAAACATGAGCTTG 3369  
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 DB 430 GCGAAGCAAAATCTCTCATTTGTGCGCTGCTCAAAAACCAAAACATGAGCTTG 371  
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 QY 3370 GTTTAAAGGATTAAGATTTCTTTTGTGTTTCTCTCAGACTTATGATATGAC 3429  
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 DB 370 GTTAAAGGATTAAGATTTCTTTTGTGTTTCTCTCAGACTTATGATATGAC 311  
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 QY 3430 GGGCTATGCAAAATTTCTATTTCTAAACTACTATGATATGACGCTGTGAG 3489  
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 DB 310 GGGCTATGCAAAATTTCTATTTCTAAACTACTATGATATGACGCTGTGAG 251  
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 QY 3490 CATATTAATTAATAATGCTGCTGCTTACAGATTAAGAGAAAAA 3534  
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 DB 250 CATATTAATTAATAATGCTGCTGCTTACAGATTAAGAGAAAAA 206  
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 A1889196  
 LOCUS t250808.x1 NCI CGAP\_Brn52 Homo sapiens cDNA clone IMAGE:2291990 3'  
 DEFINITION similar to SW:CLC3\_MOUSE P51791 CHLORIDE CHANNEL PROTEIN 3 ;, mRNA  
 sequence.  
 ACCESSION A1889196  
 VERSION A1889196  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 684)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html  
 Seq primer: -40UP from Glibco  
 High quality sequence stop: 406.  
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 Location/Qualifiers  
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 /tissue\_type="tumor, 5 pooled (see description)"  
 /lab\_host="DH10B"  
 /note="Organ: Brain; Vector: pCMV-SPO6; Site:1; Salt:  
 site:2; Note: This library represents the normalized  
 version of NCI-CGAP\_Brn52. Cloned unidirectionally.  
 Primer: Oligo dT. Average insert size 1.19 kb. Tumor  
 types include: meningioma, oligodendroglioma, astrocytoma  
 (grade II), medulloblastoma, astrocytoma (grade IV).  
 Constructed by Life Technologies."  
 BASE COUNT 166 a 151 c 150 g 217 t  
 ORIGIN  
 Query Match 17.7%; Score 641.6; DB 9; Length 684;  
 Best Local Similarity 98.5%; Pred: No. 3.3e-69;  
 Matches 658; Conservative 0; Mismatches 9; Indels 1; Gaps 1;  
 QY 1983 TTAATGGAATACCTTCTTGATGCAAAAGAAATTCATACACACCTGGCT 2042  
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 DB 684 TTAATGGAATACCTTCTTGATGCAAAAGAAATTCATACACACCTGGCT 625

QY 2043 GACGTTAGAGACCTCGAAGAAATGATCTCCCTTACGTCCTGACACAGACAATATG 2102  
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 DB 624 GACGTTAGAGACCTCGAAGAAATGATCTCCCTTACGTCCTGACACAGACAATATG 565  
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 QY 2103 ACACTGATGATATAGAAACATGATTAATGAACACGATCAATGATTTCTGTGATA 2162  
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 DB 564 ACACTGATGATATAGAAACATGATTAATGAACACGATCAATGATTTCTGTGATA 505  
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 QY 2163 ATGTCAAAAGATTCAGAGATTTAGTGGATTTCCCTCAGAAAGACCTGACAATTGCA 2222  
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 DB 504 ATGTCAAAAGATTCAGAGATTTAGTGGATTTCCCTCAGAAAGACCTGACAATTGCA 445  
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 QY 2223 ATAGAAGTGCAGG-AAAAACAGAAGGATGCTGGAGATTCCTGGGCTGTTTGGC 2281  
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 DB 444 ATAGAAGTGCAGGAAAAACAGAAGGATGCTGGAGATTTCTGGGCTGTTTGGC 385  
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 QY 2282 ACAGCAGACCCCATCTCTCCAGCAGAAAGCTCTGAGCAATTGAAGCTGCAACATTC 2341  
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 DB 384 ACAGCAGACCCCATCTCTCCAGCAGAAAGCTCTGAGCAATTGAAGCTGCAACATTC 325  
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 QY 2342 TGACATAGCCCTTTTACAGTACAGACACACCCCAATGAGATTTGTGATATTTT 2401  
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 DB 324 TGACATAGCCCTTTTACAGTACAGACACACCCCAATGAGATTCGTGTGATATTTT 265  
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 DB 264 CCGAAGCTGGAGCTGAGGAGTGCCTTGTAACTCACAATGGGGCCCTCCCTGGCATTTAT 205  
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 QY 2462 AACAAAAAAGATATCTCTCCGCGCATATGCGCCAGACGCAACCAAGCCCGCTTCAT 2521  
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 DB 204 AACAAAAAAGATATCTCTCCGCGCATATGCGCCAGACGCAACCAAGCCCGCTTCAT 145  
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 QY 2522 AATGTTCAACTGAATCTCAGAGATGAGAGAGAGAAACGGAAGGATTTATTTG 2581  
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 DB 144 AATGTTCAACTGAATCTCAGAGATGAGAGAGAGAAACGGAAGGATTTATTTG 85  
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 QY 2582 TTGAATGCACTCAACTCTTAACTGAGGAGTCACTACTTTTTCCTCCTTACAAA 2641  
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 DB 84 TTGAATGCACTCAACTCTTAACTGAGGAGTCACTACTTTTTCCTCCTTACAAA 25  
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 QY 2642 AAAAAAAA 2649  
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 DB 24 AAAAAAAA 17  
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 RESULT 15  
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 LOCUS AGENCOURT 7766456 NIH\_MGC\_68 Homo sapiens cDNA clone IMAGE:6022145  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BQ433763  
 VERSION BQ433763.1 GI:21172839  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1023)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: DCTD/DTF/Gazdar  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1AM13228 row: P column: 18  
 High quality sequence stop: 514.

## FEATURES

Location/Qualifiers

1. 1023

/organism="Homo sapiens"

/db.xref="taxon:9606"

/clone="IMAGE:6022145"

/clone\_lib="NIH-MGC\_68"

/issue\_type="large cell carcinoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: lung; Vector: PCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."

BASE COUNT 270 a 209 c 221 g 319 t 4 others

ORIGIN

Query Match 17.6%; Score 638; DB 14; length 1023;

Best Local Similarity 96.3%; Pred. No. 6,9e-69;

Matches 676; Conservative 0; Mismatches 20; Indels 6; Gaps 2;

OY 574 GGTACACACGACAGTGTGTGGGATCTAATGAACAACATTTGAAGAGGATA 633  
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Db 1 GGTACAAACGACAGACAGTGTGTGGGATCTAATGAACAACATTTGAAGAGGATA 60  
OY 634 AATGCCACAGTGGAAACATGGGAGAAATATCATAGTCAACAGCAGAGGCTCTGTT 693  
|||||  
Db 61 AATGCCACAGTGGAAACATGGGAGAAATATCATAGTCAACAGCAGAGGCTCTGTT 120  
OY 694 CTTATATCATGACATACATTAATGATCTCTGGGCTTGTAGTTTCTCTTCTTGCAG 753  
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Db 121 CTTATATCATGACATACATTAATGATCTCTGGGCTTGTAGTTTCTCTTCTTGCAG 180  
OY 754 TTTCCCTGGTAAAGGATTTCTCCATATGCTGTGCTGTGAATTCAGAGATTAA 813  
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Db 181 TTTCCCTGGTAAAGGATTTCTCCATATGCTGTGCTGTGAATTCAGAGATTAA 240  
OY 814 CTATTTTATGAGTATCTCATACAGAGTCTTGGGAAATGAGCTTAATGATTAA 873  
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Db 241 CTATTTTATGAGTATCTCATACAGAGTCTTGGGAAATGAGCTTAATGATTAA 300  
OY 874 CCATCACAATTAGTCTGCTGTGACATGAGTTTGAAGAAAGAGTCCCTG 933  
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Db 301 CCATCACAATTAGTCTGCTGTGACATGAGTTTGAAGAAAGAGTCCCTG 360  
OY 934 TACATGTTGCTGTGCTGCGGAATATCTTTCCCTTCTTCCAAAGTATAGCACA 993  
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Db 361 TACATGTTGCTGTGCTGCGGAATATCTTTCCCTTCTTCCAAAGTATAGCACA 420  
OY 994 ACGAAGCTAAAAAAGGAGGCTATCAGCTGCTCAGTCAAGGGGTTCTGTAGCT 1053  
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Db 421 ACGAAGCTAAAAAAGGAGGCTATCAGCTGCTCAGTCAAGGGGTTCTGTAGCT 480  
OY 1054 TTGGTGCACCAATTGAGAGATCTTTTACCTGGAAGAGTTAGCTATTTTCTC 1113  
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Db 481 TTGGTGCACCAATTGAGAGATCTTTTACCTGGAAGAGTTAGCTATTTTCTC 540  
OY 1114 TCAAACTTATGAGATCAATTTTGTGCTTATGAGTGCATTTGTTGAGTCCA 1173  
|||||  
Db 541 TCAAACTTATGAGATCAATTTTGTGCTTATGAGTGCATTTGTTGAGTCCA 600  
OY 1174 TCATTCATTTGTTGTTGAGAGGCTGCTGCTTTTATGT--GAGATCATACACAT 1230  
|||||  
Db 601 TCATTCATTTGTTGTTGAGAGGCTGCTGCTTTTATGTTGAGATCATACACAT 660  
OY 1231 GGTACC--TTTGAAGTCTTTCTTTATCTTTCTTGAAGG 1269  
|||||  
Db 661 GGTAACTTTTGAAGTCTTTCTTTATCTCTCCAGAG 702

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Job time : 4496 secs